

145360

From: Sullivan, Daniel
Sent: Wednesday, February 16, 2005 1:37 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request 09754014

Please search for the following in the pending, issued patent and commercial databases:

A nucleic acid comprising SEQ ID NO: 10, 13, 17 or 19

Thank you

Daniel M. Sullivan

Examiner AU 1636
Remsen Bldg.
Room 2A74

Tel: (571) 272-0779

Mailbox: 2C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 2/25/05
Date Completed: 3/2/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # 4
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 01
WWW/Internet: _____
Other(Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:40:13 ; Search time 766.446 Seconds
(without alignments)
1042.930 Million cell updates/sec

Title: US-09-754-014A-19
Perfect score: 21
Sequence: 1 tttctttctctctctcnyagg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
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2: gb_est2.*
3: gb_est3.*
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5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	18.6	88.6	327	2	BB125849 BB125849
C 4	18.6	88.6	416	9	DR3213S AL984359 DR3213S
C 5	18.4	87.6	831	9	CC535199 CC535199
C 6	18.4	85.7	347	4	B1402376 B1402376
C 7	18.4	85.7	393	4	BG541755 BG541755
C 8	18.4	85.7	409	2	AM785838 AM785838
C 9	18.4	85.7	431	5	BK557861 BK557861
C 10	18.4	85.7	482	5	B0874461 B0874461
C 11	18.4	85.7	484	8	BX993189 BX993189
C 12	18.4	85.7	500	9	CE507781 CE507781
C 13	18.4	85.7	525	1	AL682803 AL682803
C 14	18.4	85.7	526	8	AQ174755 AQ174755
C 15	18.4	85.7	537	4	B1219527 B1219527
C 16	18.4	85.7	539	8	B2277347 B2277347
C 17	18.4	85.7	541	8	A0826373 A0826373
C 18	18.4	85.7	557	9	CE518271 CE518271
C 19	18.4	85.7	562	2	BE748929 BE748929
C 20	18.4	85.7	575	9	CE569568 CE569568
C 21	18.4	85.7	590	8	A2662964 A2662964
C 22	18.4	85.7	605	8	AQ432329 AQ432329
C 23	18.4	85.7	614	8	A2443573 A2443573
C 24	18.4	85.7	660	6	CB979909 CB979909

25	18	85.7	661	8	CC433315	CC433315
26	18	85.7	662	8	AZ034000	AZ034000
27	18	85.7	690	9	CE800232	CE800232
28	18	85.7	727	8	AQ864238	AQ864238
29	18	85.7	727	8	BH933504	BH933504
30	18	85.7	735	9	CL547365	CL547365
31	18	85.7	739	9	AG414328	AG414328
32	18	85.7	755	8	CC310172	CC310172
33	18	85.7	756	2	BF792512	BF792512
34	18	85.7	756	8	AQ914105	AQ914105
35	18	85.7	776	8	BH361022	BH361022
36	18	85.7	791	8	CC366011	CC366011
37	18	85.7	799	9	CC361830	CC361830
38	18	85.7	810	8	AQ860653	AQ860653
39	18	85.7	811	4	BF966805	BF966805
40	18	85.7	813	9	CC588569	CC588569
41	18	85.7	827	5	BH359502	BH359502
42	18	85.7	858	8	B2816652	B2816652
43	18	85.7	866	8	AQ900621	AQ900621
44	18	85.7	894	9	CG363436	CG363436
45	18	85.7	906	8	B2816655	B2816655

ALIGNMENTS

RESULT 1
BG499610/c 691 bp mRNA linear EST 27-MAR-2001
LOCUS 602546774F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4669003 5',
DEFINITION mRNA sequence.

ACCESSION BG499610 GI:13461127
VERSION BG499610.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS 1 (bases 1 to 691)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LCM480 row: c column: 20
High quality sequence stop: 211.
Location/Qualifiers

FEATURES

1..691
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4669003"
/issue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgccgcgcgcgc); Site 2: SfiI (ggcgccgcgcgcgc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATATGACC-3' and 3' adaptor sequence: 5'-ATCTAGAGCCGAGCGCCGACATG-AT (30)BN-3' (where B = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto).

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:04:23 ; Search time 110.385 Seconds
(without alignments)
1127.283 Million cell updates/sec

Title: US-09-754-014A-19

Perfect score: 21
Sequence: 1 tttctttttctcttcyagg 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	19.6	93.3	160	17	US-10-400-053-7
5	19.6	93.3	160	17	US-10-419-045-13
6	19.6	93.3	3100	17	US-10-400-053-23
7	19.6	93.3	3558	18	US-10-281-067B-26
8	19.6	93.3	3558	18	US-10-764-818A-26
9	19.6	93.3	3589	15	US-10-234-406-1
10	19.6	93.3	3589	16	US-10-136-837-4
11	19.6	93.3	3609	15	US-10-234-406-3

12	19.6	93.3	4276	15	US-10-234-406-7	Sequence 7, Appl
13	19.6	93.3	4496	15	US-10-234-406-5	Sequence 5, Appl
14	19.6	93.3	4855	18	US-10-281-067B-27	Sequence 27, Appl
15	19.6	93.3	4855	18	US-10-764-818A-27	Sequence 27, Appl
16	19.6	93.3	5195	17	US-10-419-045-2	Sequence 2, Appl
17	19.6	93.3	5566	17	US-10-400-053-22	Sequence 22, Appl
18	19.6	93.3	5686	16	US-10-136-837-1	Sequence 1, Appl
19	19.6	93.3	5966	16	US-10-136-837-3	Sequence 3, Appl
20	18.6	88.6	362	17	US-10-632-117-23	Sequence 23, Appl
21	17.6	83.8	510	17	US-10-424-599-30471	Sequence 30471, A
22	17.6	83.8	921	17	US-10-335-977-4719	Sequence 4719, Ap
23	17.6	83.8	936	17	US-10-335-977-4720	Sequence 4720, Ap
24	17	81.0	201	19	US-10-741-600-25743	Sequence 25743, A
25	17	81.0	319	17	US-10-424-589-57372	Sequence 57372, A
26	17	81.0	321	18	US-10-767-701-28912	Sequence 28912, A
27	17	81.0	457	17	US-10-767-701-30036	Sequence 30036, A
28	17	81.0	464	13	US-10-027-632-40418	Sequence 40418, A
29	17	81.0	464	17	US-10-027-632-40418	Sequence 40418, A
30	17	81.0	468	10	US-09-918-995-29319	Sequence 29319, A
31	17	81.0	500	13	US-10-016-634A-92	Sequence 92, Appl
32	17	81.0	586	18	US-10-425-115-116190	Sequence 116190, A
33	17	81.0	627	18	US-10-357-930-53061	Sequence 53061, A
34	17	81.0	637	13	US-10-027-632-215696	Sequence 215696, A
35	17	81.0	637	17	US-10-027-632-215696	Sequence 215696, A
36	17	81.0	680	17	US-10-264-049-1938	Sequence 1938, Ap
37	17	81.0	713	17	US-10-424-599-127235	Sequence 127235, A
38	17	81.0	1044	9	US-09-938-842A-850	Sequence 850, App
39	17	81.0	1044	11	US-09-938-842A-850	Sequence 850, App
40	17	81.0	1145	9	US-09-984-245-99	Sequence 99, Appl
41	17	81.0	1145	10	US-09-966-262-89	Sequence 99, Appl
42	17	81.0	1145	10	US-09-983-966-89	Sequence 99, Appl
43	17	81.0	1145	14	US-10-059-395-99	Sequence 99, Appl
44	17	81.0	1145	14	US-10-143-090-99	Sequence 99, Appl
45	17	81.0	1147	13	US-10-087-192-1736	Sequence 1736, Ap

ALIGNMENTS

RESULT 1
US-09-754-014-10
; Sequence 10, Application US/09754014
; Patent No. US20020119940A1
; GENERAL INFORMATION:
; APPLICANT: Jeff No. US20020119940A1detrom
; Deepa Deshpande
; TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYSTEMS
; AND USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: PASTEPO for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,014
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/948,958
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Berkman, Charles S.

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:37:48 ; Search time 26.9231 seconds
(without alignments)
1276.296 Million cell updates/sec

Title: US-09-754-014A-19

Perfect score: 21
Sequence: 1 tctctctctctctctctcagag 21

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents NA: *
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	17.6	83.8	601	4	US-09-949-016-26038 Sequence 26038, A
3	17.6	83.8	601	4	US-09-949-016-26039 Sequence 26039, A
4	17.6	83.8	601	4	US-09-949-016-74640 Sequence 74640, A
5	17.6	83.8	601	4	US-09-949-016-74641 Sequence 74641, A
6	17.6	83.8	5599	2	US-08-477-451-9 Sequence 9, Appli
7	17.6	83.8	5599	2	US-08-477-451-13 Sequence 13, Appli
8	17.6	83.8	19932	2	US-08-477-451-25 Sequence 25, Appli
9	17.6	83.8	92334	4	US-09-949-016-13920 Sequence 13920, A
10	17.6	83.8	92363	4	US-09-949-016-12146 Sequence 12146, A
11	17.6	83.8	601	4	US-09-949-016-22416 Sequence 22416, A
12	17.6	81.0	601	4	US-09-949-016-22417 Sequence 22417, A
13	17.6	81.0	601	4	US-09-949-016-153857 Sequence 153857, A
14	17.6	81.0	601	4	US-09-949-016-154221 Sequence 154221, A
15	17.6	81.0	601	4	US-09-949-016-154222 Sequence 154222, A
16	17.6	81.0	2431	4	US-09-023-655-810 Sequence 810, App
17	17.6	81.0	3382	3	US-09-099-041A-7 Sequence 7, Appli
18	17.6	81.0	3382	3	US-09-245-281-7 Sequence 7, Appli
19	17.6	81.0	3382	3	US-09-207-359B-7 Sequence 7, Appli
20	17.6	81.0	3382	4	US-09-340-620A-7 Sequence 7, Appli
21	17.6	81.0	3382	4	US-09-865-354-7 Sequence 7, Appli
22	17.6	81.0	21857	4	US-09-949-016-12484 Sequence 12484, A
23	17.6	81.0	21938	4	US-09-949-016-17156 Sequence 17156, A
24	17.6	81.0	25190	4	US-09-949-016-15906 Sequence 15906, A
25	17.6	81.0	45365	4	US-09-949-016-11893 Sequence 11893, A
26	17.6	81.0	45456	4	US-09-949-016-17007 Sequence 17007, A
27	17.6	81.0	55827	3	US-09-813-133A-3 Sequence 3, Appli

28	17	81.0	55827	4	US-10-212-877-3 Sequence 3, Appli
29	17	81.0	64813	4	US-09-949-016-11957 Sequence 11957, A
30	17	81.0	70131	4	US-09-949-016-16064 Sequence 16064, A
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33	17	81.0	87611	4	US-09-949-016-16139 Sequence 16139, A
34	17	81.0	117001	4	US-09-949-016-15684 Sequence 15684, A
35	17	81.0	129658	4	US-09-949-016-17195 Sequence 17195, A
36	17	81.0	248968	4	US-09-949-016-12614 Sequence 12614, A
37	17	81.0	250958	4	US-09-949-016-16061 Sequence 16061, A
38	16.8	80.0	46698	4	US-09-949-016-17323 Sequence 17323, A
39	16.8	80.0	54382	4	US-09-949-016-12139 Sequence 12139, A
40	16.6	79.0	195	4	US-09-270-767-3604 Sequence 3604, Ap
41	16.6	79.0	195	4	US-09-270-767-18886 Sequence 18886, A
42	16.6	79.0	6728	4	US-09-949-016-13735 Sequence 13735, A
43	16.6	79.0	66480	4	US-09-949-016-14817 Sequence 14817, A
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45	16.6	79.0	78269	4	US-09-949-016-12497 Sequence 12497, A

ALIGNMENTS

RESULT 1
US-09-012-366-7

Sequence 7, Application US/09012366
Patent No. 6034072

GENERAL INFORMATION:

APPLICANT: Robert Ralston

APPLICANT: Susanne Muller

APPLICANT: Ruse Mumper

APPLICANT: William Munger

APPLICANT: Maria Bruno

TITLE OF INVENTION: IL-2 GENE EXPRESSION AND

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FASTSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/012,366

FILING DATE: January 23, 1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/039,709

FILING DATE: February 10, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Berkman, Charles S.

REGISTRATION NUMBER: 38,077

REFERENCE/DOCKET NUMBER: 230/214

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-012-366-7

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:30:33 ; Search time 91.7538 Seconds
(without alignments)

1354.870 Million cell updates/sec

Title: US-09-754-014A-19

Perfect score: 21
Sequence: 1 tttctttttctcttccttcnagg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq15Dec04:*
1: geneseq15908:*
2: geneseq15908:*
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13: geneseq15908:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.6	93.3	30	AAZ40413	Aaz40413 3' splice
2	19.6	93.3	30	ADP77253	Adp77253 Synthetic
3	19.6	93.3	45	AAV07276	Aav07276 Plasmid P
4	19.6	93.3	45	AAZ50395	Aaz50395 Synthetic
5	19.6	93.3	86	AAZ53801	Aaz53801 Intron #1
6	19.6	93.3	159	ADM94833	Adm94833 Synthetic
7	19.6	93.3	160	ABN86149	Abn86149 Nucleotide
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12	19.6	93.3	3100	ABN86161	Abn86161 Nucleotide
13	19.6	93.3	3308	ADL97787	Adl97787 Human foc
14	19.6	93.3	3323	ADL97788	Adl97788 Human foc
15	19.6	93.3	3334	ADL97786	Adl97786 Human foc
16	19.6	93.3	3558	AAZ60457	Aaz60457 Human foc
17	19.6	93.3	3558	ADR23406	Adr23406 Inducible
18	19.6	93.3	3589	AAZ40418	Aaz40418 Plasmid P
19	19.6	93.3	3589	AAZ70084	Aaz70084 Plasmid P
20	19.6	93.3	3589	ADP77242	Adp77242 Human IFN

21	19.6	93.3	3609	AAZ70085	Aaz70085 Plasmid P
22	19.6	93.3	4276	AAZ70087	Aaz70087 Codon opt
23	19.6	93.3	4496	AAZ70086	Aaz70086 Plasmid P
24	19.6	93.3	4855	AAZ60458	Aaz60458 Nucleic-sp
25	19.6	93.3	4855	AAZ53818	Aaz53818 Nucleic-sp
26	19.6	93.3	4855	ADR23407	Adr23407 Nucleic-sp
27	19.6	93.3	5195	ABQ74554	Abq74554 Human Del
28	19.6	93.3	5195	ADM94827	Adm94827 Human dev
29	19.6	93.3	5566	ABN86160	Abn86160 Nucleotide
30	19.6	93.3	5686	AAZ40415	Aaz40415 Plasmid P
31	19.6	93.3	5686	ADP77239	Adp77239 Human IL-
32	19.6	93.3	5966	AAZ40417	Aaz40417 Plasmid P
33	19.6	93.3	5966	ADP77241	Adp77241 Mouse IL-
34	18.6	88.6	362	ABZ59810	Abz59810 Streptoco
35	17.6	83.8	495	AAZ75463	Aaz75463 Human ORF
36	17.6	83.8	19932	AAZ46159	Aaz46159 Cagl locu
37	17.6	83.8	201	ADS39455	Ads39455 Human aut
38	17.6	83.8	201	ADS38124	Ads38124 Human aut
39	17.6	83.8	468	ACH42107	Ach42107 Human fce
40	17.6	83.8	500	ABV94001	Abv94001 Human COL
41	17.6	83.8	552	AAH12056	Aah12056 Human CDN
42	17.6	83.8	627	ABV53042	Abv53042 Human pro
43	17.6	83.8	680	ABQ56058	Abq56058 Human ova
44	17.6	83.8	778	AAZ94487	Aaz94487 Human fce
45	17.6	83.8	1044	ABZ13045	Abz13045 Arabidops

ALIGNMENTS

RESULT 1	AAZ40413	standard; DNA; 30 BP.
ID	AAZ40413	
XX	AAZ40413;	
AC	AAZ40413;	
XX	AAZ40413;	
DT	15-FEB-2000 (first entry)	
XX	15-FEB-2000 (first entry)	
DE	3' splice site sequence for interferon-alpha plasmid.	
XX	3' splice site sequence for interferon-alpha plasmid.	
KW	Wild type; human; interferon-alpha; plasmid; cytomegalovirus; CMV;	
KM	promoter; growth hormone; untranslated region; UTR; mammal; disease;	
KW	cancer; Intron; ss.	
OS	Synthetic.	
XX	Synthetic.	
PN	MO9947678-A2.	
XX	MO9947678-A2.	
PD	23-SEP-1999.	
XX	23-SEP-1999.	
PF	12-MAR-1999; 99WO-US005394.	
XX	12-MAR-1999; 99WO-US005394.	
PR	19-MAR-1998; 98US-0078654P.	
XX	19-MAR-1998; 98US-0078654P.	
PA	(GENE-) GENEMEDICINE INC.	
XX	(GENE-) GENEMEDICINE INC.	
PI	Nordstrom J, Pericle F, Rolland A, Ralston R;	
XX	Nordstrom J, Pericle F, Rolland A, Ralston R;	
DR	WPI; 1999-562116/47.	
XX	WPI; 1999-562116/47.	
PT	New plasmids containing an interferon-alpha coding sequence, used for the	
PT	treatment of a mammalian condition or disease, particularly cancer.	
XX	treatment of a mammalian condition or disease, particularly cancer.	
PS	Disclosure; Page 31; 137pp; English.	
XX	Disclosure; Page 31; 137pp; English.	
CC	The invention relates to a novel plasmid comprising a cytomegalovirus	
CC	(CMV) promoter transcriptionally linked with an interferon alpha (IFN-	
CC	alpha) coding sequence, and a growth hormone 3'-untranslated region	
CC	(UTR). Sequences AAZ40412 and AAZ40413 represent synthetic 5' and 3'	
CC	splice donor and acceptor sites respectively for generating a synthetic	
CC	intron to be inserted into the plasmid of the invention. The plasmids can	
CC	be used for treating a mammalian condition or disease, particularly	
CC	cancer	

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OM nucleic - nucleic search, using SW model

Run on: March 1, 2005, 12:35:38 ; Search time 346.877 Seconds
(without alignments)
2933.489 Million cell updates/sec

Title: US-09-754-014A-19

Perfect score: 21

Sequence: 1 tttctttttctctcttcnnyagg 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank1:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.6	93.3	30	BD136046	BD136046 Interfero
2	19.6	93.3	30	BD069111	BD069111 IL-2 gene
3	19.6	93.3	45	BD272241	BD272241 Anti-angi
4	19.6	93.3	45	BD007073	BD007073 IL-12 gen
5	19.6	93.3	45	BD007083	BD007083 Gene exp
6	19.6	93.3	86	AX451627	AX451627 Sequence
7	19.6	93.3	160	AX451629	AX451629 Sequence
8	19.6	93.3	3100	AX451645	AX451645 Sequence
9	19.6	93.3	3589	CQ854738	CQ854738 Sequence
10	19.6	93.3	3589	BD136051	BD136051 Interfero
11	19.6	93.3	3589	AX249943	AX249943 Sequence
12	19.6	93.3	3609	AX249944	AX249944 Sequence
13	19.6	93.3	4276	AX249946	AX249946 Sequence
14	19.6	93.3	4486	AX249945	AX249945 Sequence
15	19.6	93.3	4855	CQ854739	CQ854739 Sequence
16	19.6	93.3	5566	AX451644	AX451644 Sequence
17	19.6	93.3	5566	BD136048	BD136048 Interfero
18	19.6	93.3	5966	BD136050	BD136050 Interfero
19	19.6	93.3	128765	HUAC002040	AC002040 Homo sapi

20	19.6	93.3	172331	9	AC127459	AC127459 Homo sapi
21	19.6	93.3	203668	2	AC084411	AC084411 Mus muscu
22	18.6	88.6	362	1	AF302194	AF302194 Streptoco
23	18.6	88.6	362	6	AX528956	AX528956 Sequence
24	18.6	88.6	39573	3	L23645	L23645 Caenorhabd
25	18.6	88.6	157690	8	CNS08CA3	AL772425 Oryza sat
26	18.6	88.6	172477	2	AY707984	AY707984 Oryza sat
27	18.6	88.6	191512	2	AY914207	BX914207 Dario rer
28	18.6	88.6	239843	2	AC15518	AC15518 Rattus no
29	18.6	88.6	254686	2	AC126140	AC126140 Rattus no
30	18.4	87.6	161868	2	AC007241	AC007241 Homo sapi
31	18.4	87.6	175140	2	AC064823	AC064823 Homo sapi
32	18.4	87.6	176780	9	AC015978	AC015978 Homo sapi
33	18	85.7	3994	10	EX321866	EX321866 Mouse DNA
34	18	85.7	16753	2	AC151769	Continuation (5 of
35	18	85.7	38953	9	AL360075	AL360075 Human DNA
36	18	85.7	49457	2	AC104261	AC104261 Homo sapi
37	18	85.7	57051	2	AC100297	AC100297 Mus muscu
38	18	85.7	67675	2	AC021389	AC021389 Homo sapi
39	18	85.7	67980	2	AC108669	AC108669 Homo sapi
40	18	85.7	70559	2	AC101425	AC101425 Mus muscu
41	18	85.7	75874	2	SPNEU1907	AL449929 Streptoco
42	18	85.7	79111	5	EX927172	EX927172 Zebralfish
43	18	85.7	87500	9	AC022513	AC022513 Homo sapi
44	18	85.7	98424	8	AC148238	AC148238 Medicago
45	18	85.7	121483	4	EX323833	EX323833 Pig DNA

ALIGNMENTS

RESULT 1
BD136046
LOCUS
DEFINITION
Interferon alpha plasmid and delivery system and method of
preparing and using the same.
BD136046
ACCESSION
BD136046.1 GI:23230991
VERSION
JP 2002506647-A/13.
KEYWORDS
SOURCE
ORGANISM
other sequences: artificial sequences.
REFERENCE
1 (bases 1 to 30)
Nordstrom,J., Pericle,F., Rolland,A. and Ralston,R.
Interferon alpha plasmid and delivery system and method of
preparing and using the same
Patient: JP 2002506647-A 13 05-MAR-2002;
JOURNAL
VALENTIS INC
COMMENT
OS Artificial Sequence
PN JP 2002506647-A/13
PD 05-MAR-2002
PR 12-MAR-1999 JP 2000536861
PI 19-MAR-1998 US 60/078654
PC JEFF NORDSTROM, FEDERICA PERICLE, ALAIN ROLLAND, ROBERT RALSTON
PC C12N15/09, A61K38/21, A61K48/00, A61P35/00, C07K14/54, C07K14/56,
PC C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10//A61K9/127, C12N15/00, A61K37/66, PC
C12N5/00
CC Sequence source: synthetic construct
FH key
FT source
FT location/Qualifiers
1. .30
/organism="Artificial Sequence".
location/Qualifiers
1. .30
/mol_type="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES

source

ORIGIN

Query Match 93.3%; Score 19.6; DB 6; Length 30;
Best Local Similarity 90.5%; Pred. No. 6.2e+02;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:40:13 ; Search time 255.482 Seconds
(without alignments)
1042.930 Million cell updates/sec

Title: US-09-754-014a-17

Perfect score: 7

Sequence: 1 taccac 7

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_ests1:*
2: gb_ests2:*
3: gb_hic:*
4: gb_ests3:*
5: gb_ests4:*
6: gb_ests5:*
7: gb_ests6:*
8: gb_g881:*
9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	19	7	CO786076
2	7	100.0	19	8	AZ623493
3	7	100.0	19	8	AZ778302
4	7	100.0	19	8	AZ806669
5	7	100.0	21	8	AZ812861
6	7	100.0	22	8	AZ851620
7	7	100.0	23	7	CF308058
8	7	100.0	23	8	AZ476882
9	7	100.0	23	9	AG189480
10	7	100.0	23	9	TA164G120
11	7	100.0	23	6	CD744129
12	7	100.0	24	8	AZ304717
13	7	100.0	25	8	BH910894
14	7	100.0	25	8	BZ381299
15	7	100.0	25	9	CG718650
16	7	100.0	25	9	CG718650
17	7	100.0	26	8	AZ364052
18	7	100.0	27	8	AZ351430
19	7	100.0	28	8	AZ609297
20	7	100.0	28	8	BH863505
21	7	100.0	28	9	AJ587873
22	7	100.0	28	8	BH910847
23	7	100.0	29	8	AZ480938
24	7	100.0	30	8	AZ480938

25	7	100.0	30	8	AZ591759	AZ591759
26	7	100.0	30	8	AZ857764	AZ857764
27	7	100.0	30	9	AL762304	AL762304
28	7	100.0	30	9	DR19035	DR19035
29	7	100.0	31	2	AV960314	AV960314
30	7	100.0	31	2	AV960314	AV960314
31	7	100.0	31	8	AZ318049	AZ318049
32	7	100.0	31	9	CG718776	CG718776
33	7	100.0	32	8	AZ387853	AZ387853
34	7	100.0	32	8	AZ391582	AZ391582
35	7	100.0	32	8	AZ605009	AZ605009
36	7	100.0	32	8	BH852695	BH852695
37	7	100.0	32	8	BH854186	BH854186
38	7	100.0	32	8	BH904979	BH904979
39	7	100.0	32	8	TA253H10P	TA253H10P
40	7	100.0	33	8	AZ769247	AZ769247
41	7	100.0	33	8	BZ358044	BZ358044
42	7	100.0	33	9	AL766917	AL766917
43	7	100.0	33	9	TA227D090	TA227D090
44	7	100.0	33	9	TA364B10P	TA364B10P
45	7	100.0	34	1	AU256929	AU256929

ALIGNMENTS

RESULT 1
LOCUS CO786076
DEFINITION BL285B E05 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum
CDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION CO786076.1 GI:5102056
VERSION
KEYWORDS
SOURCE
ORGANISM Ambystoma mexicanum (axolotl)
Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomidae;
Ambystoma.
1 (bases 1 to 19)
Habelmann, B., Beblin, A.G., Herklitz, S., Volkmann, M., Eckelt, K.,
Pelke, K., Epperlein, H.H., Schachert, H.K., Wiebe, G. and Tanaka, E.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. (2004) In press
Contact: Ely M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfeifferhauserstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL285B row: 05 column: E
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
1..19
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Tail Blastema"
/cell_type="regenerating tail blastema"
/clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
/note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unmutagenized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was poly(A) tailed and cloned into
EMD108-TONA. Bacterial host is
EMD108-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DAXBL"

ORIGIN

Query Match 100.0%; Score 7; DB 7; Length 19;

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:04:23 ; Search time 36.7949 Seconds
(without alignments)
1127.283 Million cell updates/sec

Title: US-09-754-014a-17

Perfect score: 7
Sequence: 1 tactaac 7

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	US-10-400-053-3	Sequence 3, Appl1
2	7	100.0	7	US-10-419-045-11	Sequence 11, Appl1
3	7	100.0	7	US-10-198-447A-24	Sequence 24, Appl1
4	7	100.0	7	US-10-333-914-6	Sequence 6, Appl1
5	7	100.0	7	US-10-374-784A-3	Sequence 3, Appl1
6	7	100.0	7	US-10-621-867-24	Sequence 24, Appl1
7	7	100.0	10	US-10-033-145-942	Sequence 942, App
8	7	100.0	10	US-10-225-501-3	Sequence 3, Appl1
9	7	100.0	11	US-10-149-109A-27	Sequence 27, Appl1
10	7	100.0	11	US-10-149-109A-28	Sequence 28, Appl1
11	7	100.0	12	US-10-257-017B-267651	Sequence 267651,

12	7	100.0	12	US-10-257-017B-267994	Sequence 267994,
13	7	100.0	12	US-10-257-017B-268138	Sequence 268138,
14	7	100.0	12	US-10-257-017B-268269	Sequence 268269,
15	7	100.0	12	US-10-257-017B-269417	Sequence 269417,
16	7	100.0	12	US-10-257-017B-269425	Sequence 269425,
17	7	100.0	12	US-10-257-017B-269953	Sequence 269953,
18	7	100.0	12	US-10-257-017B-270179	Sequence 270179,
19	7	100.0	12	US-10-257-017B-271344	Sequence 271344,
20	7	100.0	12	US-10-257-017B-271630	Sequence 271630,
21	7	100.0	12	US-10-257-017B-272883	Sequence 272883,
22	7	100.0	12	US-10-257-017B-272847	Sequence 272847,
23	7	100.0	12	US-10-257-017B-272997	Sequence 272997,
24	7	100.0	12	US-10-257-017B-274276	Sequence 274276,
25	7	100.0	12	US-10-257-017B-274934	Sequence 274934,
26	7	100.0	12	US-10-257-017B-275558	Sequence 275558,
27	7	100.0	12	US-10-257-017B-276558	Sequence 276558,
28	7	100.0	12	US-10-257-017B-276869	Sequence 276869,
29	7	100.0	12	US-10-257-017B-277250	Sequence 277250,
30	7	100.0	12	US-10-257-017B-277367	Sequence 277367,
31	7	100.0	12	US-10-257-017B-277368	Sequence 277368,
32	7	100.0	12	US-10-257-017B-277907	Sequence 277907,
33	7	100.0	12	US-10-257-017B-278347	Sequence 278347,
34	7	100.0	12	US-10-257-017B-278659	Sequence 278659,
35	7	100.0	12	US-10-257-017B-278660	Sequence 278660,
36	7	100.0	12	US-10-257-017B-278969	Sequence 278969,
37	7	100.0	12	US-10-257-017B-279336	Sequence 279336,
38	7	100.0	12	US-10-257-017B-279420	Sequence 279420,
39	7	100.0	12	US-10-257-017B-279421	Sequence 279421,
40	7	100.0	12	US-10-257-017B-279748	Sequence 279748,
41	7	100.0	12	US-10-257-017B-280030	Sequence 280030,
42	7	100.0	12	US-10-257-017B-280031	Sequence 280031,
43	7	100.0	12	US-10-257-017B-280215	Sequence 280215,
44	7	100.0	12	US-10-257-017B-280345	Sequence 280345,
45	7	100.0	12	US-10-257-017B-284147	Sequence 284147,

ALIGNMENTS

RESULT 1
US-10-400-053-3
Sequence 3, Application US/10400053
Publication No. US20030220286A1
GENERAL INFORMATION:
APPLICANT: Abnuzese, Ronald V
APPLICANT: Mehta, Vidya
APPLICANT: No. US20030220286A1dstrom, Jeffrey L
APPLICANT: Fewell, Jason
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Improved System for Regulation of Transgene Expression
FILE REFERENCE: 213-0080US
CURRENT APPLICATION NUMBER: US/10/400,053
PRIOR FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: PCT/US01/30305
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/260,781
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/278,281
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/235,030
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 3
LENGTH: 7
TYPES: RNA
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: branch point sequence for a synthetic intron
US-10-400-053-3
Query Match 100.0%; Score 7; DB 17; Length 7;

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:37:48 ; Search time 8.97436 Seconds
(without alignments)
1276.296 Million cell updates/sec

Title: US-09-754-014a-17

Perfect score: 7

Sequence: 1 taccac 7

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/6C_COMB.seq:*
6: /cgn2_6/prodata/1/ina/6D_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	US-09-403-267-1	Sequence 1, Appli
2	7	100.0	7	US-09-349-740A-8	Sequence 8, Appli
3	7	100.0	9	US-08-646-789A-63	Sequence 63, Appli
4	7	100.0	12	US-08-607-078-5	Sequence 5, Appli
5	7	100.0	12	US-09-403-267-33	Sequence 33, Appli
6	7	100.0	12	US-09-359-921-5	Sequence 5, Appli
7	7	100.0	12	US-09-360-344-5	Sequence 5, Appli
8	7	100.0	13	US-08-148-058A-2	Sequence 2, Appli
9	7	100.0	13	US-08-478-042-2	Sequence 2, Appli
10	7	100.0	13	US-08-645-213-2	Sequence 2, Appli
11	7	100.0	13	US-08-466-604-2	Sequence 2, Appli
12	7	100.0	14	US-08-297-808A-4	Sequence 4, Appli
13	7	100.0	15	US-09-242-690A-16	Sequence 16, Appli
14	7	100.0	15	US-09-908-855-16	Sequence 16, Appli
15	7	100.0	16	US-09-731-466-4	Sequence 4, Appli
16	7	100.0	16	US-09-474-432B-3	Sequence 3, Appli
17	7	100.0	16	US-09-476-387-3	Sequence 4, Appli
18	7	100.0	16	US-09-476-387-3	Sequence 4, Appli
19	7	100.0	17	US-07-990-965-3	Sequence 3, Appli
20	7	100.0	17	US-08-758-306-347	Sequence 347, App
21	7	100.0	17	US-08-758-306-349	Sequence 349, App
22	7	100.0	17	US-08-758-306-351	Sequence 351, App
23	7	100.0	17	US-08-758-306-351	Sequence 351, App
24	7	100.0	17	US-08-758-306-1315	Sequence 1315, Ap
25	7	100.0	17	US-08-758-306-1317	Sequence 1317, Ap
26	7	100.0	17	US-08-758-306-1319	Sequence 1319, Ap
27	7	100.0	17	US-08-758-306-1321	Sequence 1321, Ap

28	7	100.0	17	US-09-731-466-5	Sequence 5, Appli
29	7	100.0	17	US-09-479-279-5	Sequence 5, Appli
30	7	100.0	17	US-09-479-279-5	Sequence 6, Appli
31	7	100.0	18	US-08-683-743-19	Sequence 19, Appli
32	7	100.0	18	US-08-810-559-65	Sequence 65, Appli
33	7	100.0	18	US-08-784-582-63	Sequence 63, Appli
34	7	100.0	18	US-08-413-740A-152	Sequence 152, App
35	7	100.0	18	US-09-334-938-20	Sequence 20, Appli
36	7	100.0	18	US-09-649-747A-50	Sequence 50, Appli
37	7	100.0	18	US-09-422-978-10632	Sequence 708, Ap
38	7	100.0	18	US-09-422-978-10632	Sequence 10632, A
39	7	100.0	18	PCT-US95-04063-152	Sequence 152, App
40	7	100.0	19	US-08-219-842-24	Sequence 24, Appli
41	7	100.0	19	US-08-066-325-20	Sequence 20, Appli
42	7	100.0	19	US-08-451-056-24	Sequence 24, Appli
43	7	100.0	19	US-08-483-695-15	Sequence 15, Appli
44	7	100.0	19	US-07-965-285-15	Sequence 15, Appli
45	7	100.0	19	US-08-487-231-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-09-403-267-1
Sequence 1, Application US/09403267
Patent No. 6159710
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy, and Biology
APPLICANT: Fraser, Nigel W.
APPLICANT: Zabolotny, Janice M.
APPLICANT: Krumenacher, Claude F.
TITLE OF INVENTION: Method and Compositions for Stabilizing
TITLE OF SEQUENCES: Unstable Gene Transcripts
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/403,267
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,664
FILING DATE: 18-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST78APCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: RNA (genomic)
US-09-403-267-1
Query Match 100.0%; Score 7; DB 3; Length 7;
Best Local Similarity 71.4%; Pred. No. 2.3e+08;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:30:33 ; Search time 30.5846 Seconds
(without alignments)
1354.870 Million cell updates/sec

Title: US-09-754-014A-17

Perfect score: 7

Sequence: 1 tctaac 7

Scoring table:

IDENTITY NUC
dapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseq19808:.*
2: Geneseq19908:.*
3: Geneseq20008:.*
4: Geneseq20018:.*
5: Geneseq20018:.*
6: Geneseq20028:.*
7: Geneseq20028:.*
8: Geneseq20038:.*
9: Geneseq20038:.*
10: Geneseq20038:.*
11: Geneseq20048:.*
12: Geneseq20048:.*
13: Geneseq20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	2	AAV43560 Insertion
2	7	100.0	7	2	AAV43552 Insertion
3	7	100.0	7	2	AAV64932 int
4	7	100.0	9	12	ADK14323 Candida p
5	7	100.0	10	3	AAZ78514 Human den
6	7	100.0	10	3	AAZ81140 Metatracti
7	7	100.0	10	5	AAAF41210 Yeast NOR
8	7	100.0	10	5	AAAF43472 Yeast NOR
9	7	100.0	10	5	AAAF42417 Yeast NOR
10	7	100.0	10	5	AAAF41530 Yeast NOR
11	7	100.0	10	5	AAAF42338 Yeast NOR
12	7	100.0	10	6	ABK86389 Human SA
13	7	100.0	10	8	ABZ81783 HCV 5' UT
14	7	100.0	11	4	AAH55245 Genomic D
15	7	100.0	11	4	AAH55245 Genomic D
16	7	100.0	11	4	AAH55245 Genomic D
17	7	100.0	11	4	AAH55246 Genomic D
18	7	100.0	12	3	AAZ98509 Target se
19	7	100.0	12	3	AAZ98509 Nucleotid
20	7	100.0	12	3	AAZ98509 Nucleotid

C	21	7	100.0	12	5	AB117485	Ab117485 Oligonuc1
C	22	7	100.0	12	5	ABH68017	AbH68017 Oligonuc1
C	23	7	100.0	12	5	ABH69440	AbH69440 Oligonuc1
C	24	7	100.0	12	5	ABH95945	AbH95945 Oligonuc1
C	25	7	100.0	12	5	AB121817	Ab121817 Oligonuc1
C	26	7	100.0	12	5	ABH98712	AbH98712 Oligonuc1
C	27	7	100.0	12	5	ABH99910	AbH99910 Oligonuc1
C	28	7	100.0	12	5	AB128442	Ab128442 Oligonuc1
C	29	7	100.0	12	5	AB128534	Ab128534 Oligonuc1
C	30	7	100.0	12	5	ABH79343	AbH79343 Oligonuc1
C	31	7	100.0	12	5	AB129813	Ab129813 Oligonuc1
C	32	7	100.0	12	5	ABH80037	AbH80037 Oligonuc1
C	33	7	100.0	12	5	AB105591	Ab105591 Oligonuc1
C	34	7	100.0	12	5	AB105688	Ab105688 Oligonuc1
C	35	7	100.0	12	5	AB132759	Ab132759 Oligonuc1
C	36	7	100.0	12	5	AB108415	Ab108415 Oligonuc1
C	37	7	100.0	12	5	AB135069	Ab135069 Oligonuc1
C	38	7	100.0	12	5	ABH87227	AbH87227 Oligonuc1
C	39	7	100.0	12	5	AB112652	Ab112652 Oligonuc1
C	40	7	100.0	12	5	AB138553	Ab138553 Oligonuc1
C	41	7	100.0	12	5	AB141173	Ab141173 Oligonuc1
C	42	7	100.0	12	5	AB142237	Ab142237 Oligonuc1
C	43	7	100.0	12	5	AB149567	Ab149567 Oligonuc1
C	44	7	100.0	12	5	AB151546	Ab151546 Oligonuc1
C	45	7	100.0	12	5	AB168913	Ab168913 Oligonuc1

ALIGNMENTS

RESULT 1
ID AAV43560 standard; DNA; 7 BP.
XX
AC AAV43560;
XX
DT 25-MAR-2003 (revised)
DT 16-SEP-1998 (first entry)
XX
DE Insertion sequence 13 used for creating a tagged gene.
XX
OS Tagged gene; tagged transcript; hybrid inton; protein tag;
XX protein isolation; recombination; subcellular structure analysis;
XX transcripional regulation; viral infection; ss.
XX
OS Synthetic.
XX Unidentified.
XX
PN WO9820031-A1.
XX
PD 14-MAY-1998.
XX
PF 07-NOV-1997; 97WO-US020150.
XX
PR 08-NOV-1996; 96US-00745404.
XX
PA (JARV/) JARVIK J W.
XX
PI Jarvik JW;
XX
XX WPI; 1998-286861/25.
XX
PT Tagging genes, transcripts and proteins - using tag-creating DNA inserted
PT into inton of gene to create 2 hybrid introns separated by new exon
PT encoding protein tag.
XX
PS Claim 1; Page 33; 66pp; English.
XX
CC This sequence is used in the method of invention for tagging genes,
CC transcripts and proteins in cells in a single recombinational event. The
CC method comprises producing a tagged gene by inserting a DNA sequence into
CC an inton of a gene by selecting a DNA sequence having a 5' portion free
CC of any nucleotide sequence selected from AAV43548 to AAV43551, a

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:35:38 ; Search time 115.626 Seconds
(without alignments)
2933.489 Million cell updates/sec

Title: US-09-754-014A-17

Perfect score: 1 tctaac 7

Sequence: 1 tctaac 7

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_srs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	6	AX203149 Sequence
2	7	100.0	7	6	AX451625 Sequence
3	7	100.0	7	6	AX770099 Sequence
4	7	100.0	10	6	BD239524 Sequence
5	7	100.0	11	6	AX175038 Sequence
6	7	100.0	11	6	AX175039 Sequence
7	7	100.0	12	6	AR121253 Sequence
8	7	100.0	12	6	AR305536 Sequence
9	7	100.0	12	6	AR455354 Sequence
10	7	100.0	13	6	AR037996 Sequence
11	7	100.0	13	6	AR039094 Sequence
12	7	100.0	13	6	AR050339 Sequence
13	7	100.0	14	6	AR062898 Sequence
14	7	100.0	15	6	BD208263 Sequence
15	7	100.0	15	6	BD208264 Sequence
16	7	100.0	15	6	BD208265 Enzymatic
17	7	100.0	15	6	BD208265 Enzymatic
18	7	100.0	15	6	AR382531 Sequence
19	7	100.0	15	6	AX587026 Sequence

20	7	100.0	16	6	AR211428 Sequence
21	7	100.0	16	6	AR285631 Sequence
22	7	100.0	16	6	AR285632 Sequence
23	7	100.0	16	6	AR397622 Sequence
24	7	100.0	16	6	AR397623 Sequence
25	7	100.0	17	6	AR039489 Sequence
26	7	100.0	17	6	AR039501 Sequence
27	7	100.0	17	6	AR039503 Sequence
28	7	100.0	17	6	AR040467 Sequence
29	7	100.0	17	6	AR040469 Sequence
30	7	100.0	17	6	AR040471 Sequence
31	7	100.0	17	6	AR040473 Sequence
32	7	100.0	17	6	BD201647 Method an
33	7	100.0	17	6	BD201648 Method an
34	7	100.0	17	6	BD201649 Method an
35	7	100.0	17	6	BD201650 Method an
36	7	100.0	17	6	E01964 DNA encodin
37	7	100.0	17	6	E03611 DNA primer
38	7	100.0	17	6	I26214 Sequence 3
39	7	100.0	17	6	AR211429 Sequence
40	7	100.0	17	6	AR213616 Sequence
41	7	100.0	17	6	AR451587 Sequence
42	7	100.0	17	6	AR451588 Sequence
43	7	100.0	17	6	AX214703 Sequence
44	7	100.0	17	6	AX214704 Sequence
45	7	100.0	17	6	AX214705 Sequence

ALIGNMENTS

RESULT 1	AX203149	AX203149	7 bp	mRNA	linear	PAT 30-AUG-2001
LOCUS	AX203149	Sequence 2 from Patent WO0153529.				
DEFINITION	AX203149					
ACCESSION	AX203149					
VERSION	AX203149.1	GI:15392500				
KEYWORDS						
SOURCE						
ORGANISM						
synthetic construct						
other sequences; artificial sequences.						
1 (bases 1 to 7)						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
Genome Therapeutics Corporation (US)						
Location/Qualifiers						
1..7						
/organism="synthetic construct"						
/mol_type="mRNA"						
/db_xref="taxon:32630"						
/note="Yeast consensus branch site"						
ORIGIN						
Query Match						
Best Local Similarity						
Matches						
100.0%; Score 7; DB 6; Length 7;						
100.0%; Pred. No. 6.9e+09; Indels						
7; Conservative 0; Mismatches 0; Gaps 0;						
Qy						
1 TACTAAC 7						
1 TACTAAC 7						
Db						
RESULT 2						
AX451625						
LOCUS						
DEFINITION						
ACCESSION						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
synthetic construct						
other sequences; artificial sequences.						
AX451625						
Sequence 3 from Patent WO0224899.						
AX451625						
GI:21698567						
AX451625						
7 bp						
mRNA						
linear						
PAT 03-JUL-2002						

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:40:13 ; Search time 4452.69 Seconds
(without alignment)
1042.930 Million cell updates/sec

Title: US-09-754-014A-13

Title score: 122
Sequence: 1 caggtacgtcctccnnnn.....tctttctctctccacagg 122

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_esc1:
2: gb_esc2:
3: gb_hic:
4: gb_esc3:
5: gb_esc4:
6: gb_esc5:
7: gb_esc6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26.8	22.0	510	2	BB693146 BB693146
2	26.8	22.0	517	5	BY480596 BY480596
3	26.2	21.5	384	9	CNS00MCO
4	26.2	21.5	656	8	B27635
5	25.8	21.1	851	6	CA971907
6	25.6	21.0	594	6	AZ156400
7	25.4	20.8	444	6	CB831948
8	25.4	20.8	672	9	AG107479
9	25.5	20.5	945	4	CNS04LH3
10	24.8	20.3	820	4	BG355213
11	24.8	20.3	1101	9	CNS00LCO
12	24.6	20.2	1101	9	CNS00LST
13	24.6	20.2	459	8	AQ064274
14	24.6	20.2	479	2	BFS16085
15	24.6	20.2	514	6	CA389438
16	24.6	20.2	553	4	BM755941
17	24.6	20.2	746	6	CD104639
18	24.6	20.2	803	6	CD522232
19	24.6	20.2	870	7	CN842612
20	24.6	20.2	898	5	BU178252
21	24.6	20.2	966	8	CC410804
22	24.6	20.2	1111	4	BM801811
23	24.6	20.2	1331	3	CR600105
24	24.4	20.0	246	8	BH343677

25	24.4	20.0	437	9	FR0017265
26	24.4	20.0	794	4	BL131955
27	24.4	20.0	1020	8	CC258042
28	24.2	19.8	901	9	CNS0484E
29	24.2	19.8	952	9	CNS048IX
30	24	19.7	468	5	BK498586
31	24	19.7	505	2	AM637524
32	24	19.7	631	5	BK645475
33	24	19.7	657	9	BK199394
34	24	19.7	684	6	CB973125
35	24	19.7	703	9	CE716387
36	24	19.7	858	2	BE387547
37	24	19.7	873	2	BB889025
38	24	19.7	879	5	BQ35374
39	24	19.7	889	5	BQ10266
40	24	19.7	960	4	BG251071
41	24	19.7	970	8	CC240074
42	23.8	19.5	244	8	AQ047347
43	23.8	19.5	371	7	CP938697
44	23.8	19.5	417	1	AL653017
45	23.8	19.5	461	7	CF422456

ALIGNMENTS

RESULT 1	BB693146	510 bp	mRNA	linear	EST 10-OCT-2001
LOCUS	BB693146				
DEFINITION	BB693146 RIKEN full-length enriched, 2 days neonate sympathetic ganglion Mus musculus cDNA clone 7120442C01 3', mRNA sequence.				
ACCESSION	BB693146.1	GI:16019879			
VERSION					
KEYWORDS					
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE					
AUTHORS	Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hirozane, T., Imoto, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Kono, H., Konda, M., Matsuyama, T., Nakamura, M., Nishii, K., Nomura, K., Numasaki, R., Otsaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Watabiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.				

TITLE

JOURNAL COMMENT

Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:04:23 ; Search time 641.282 Seconds
(without alignments)

1127.283 Million cell updates/sec

Title: us-09-754-014A-13

Perfect score: 122

Sequence: 1 cagcgaagcagctctcmmmm.....tcttttctctccacag 122

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	45	36.9	3558	US-10-281-067B-26	Sequence 26, Appl
3	45	36.9	3558	US-10-764-818A-26	Sequence 26, Appl
4	45	36.9	3589	US-10-234-406-1	Sequence 1, Appl
5	45	36.9	3589	US-10-136-837-4	Sequence 4, Appl
6	45	36.9	3609	US-10-234-406-3	Sequence 3, Appl
7	45	36.9	4276	US-10-234-406-7	Sequence 7, Appl
8	45	36.9	4496	US-10-234-406-5	Sequence 5, Appl
9	45	36.9	4855	US-10-281-067B-27	Sequence 27, Appl
10	45	36.9	4855	US-10-764-818A-27	Sequence 27, Appl
11	45	36.9	5195	US-10-419-045-2	Sequence 2, Appl

12	45	36.9	5566	17	US-10-400-053-22	Sequence 22, Appl
13	45	36.9	5586	16	US-10-136-837-1	Sequence 1, Appl
14	45	36.9	5596	16	US-10-136-837-3	Sequence 3, Appl
15	45	27.9	160	17	US-10-400-053-7	Sequence 7, Appl
16	34	27.9	160	17	US-10-419-045-13	Sequence 13, Appl
17	30	24.6	45	9	US-09-754-014-10	Sequence 10, Appl
18	30	24.6	45	9	US-09-836-866-6	Sequence 6, Appl
19	28	23.0	86	17	US-10-400-053-5	Sequence 5, Appl
20	26	21.3	1399	17	US-10-369-493-29964	Sequence 29964, A
21	25.4	20.8	201	18	US-10-719-993-30427	Sequence 30427, A
22	25.4	20.8	4602	10	US-09-809-391-74	Sequence 74, Appl
23	25.4	20.8	4602	10	US-09-882-171-74	Sequence 74, Appl
24	25.4	20.8	4602	17	US-10-164-861-74	Sequence 74, Appl
25	25.4	20.8	775062	18	US-10-719-993-6844	Sequence 6844, Ap
26	24.8	20.3	2318	18	US-10-357-930-28435	Sequence 28435, A
27	24.6	20.2	975	18	US-10-425-115-165294	Sequence 165294, A
28	24.6	20.2	2786	10	US-09-809-391-238	Sequence 238, App
29	24.6	20.2	2786	10	US-09-882-171-238	Sequence 238, App
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35	24	19.7	32188	14	US-10-074-095-799	Sequence 799, App
36	24	19.7	32188	17	US-10-212-872-799	Sequence 799, App
37	24	19.7	180227	18	US-10-322-281-308	Sequence 308, App
38	23.8	19.5	2088	10	US-09-814-353-19402	Sequence 19402, A
39	23.8	19.5	344548	13	US-10-087-192-334	Sequence 334, App
40	23.6	19.3	546025	18	US-10-719-993-6862	Sequence 6862, A
41	23.4	19.2	214405	13	US-10-027-632-76212	Sequence 76212, A
42	23.4	19.2	214405	17	US-10-027-632-76212	Sequence 76212, A
43	23.2	19.0	734	13	US-10-027-632-28194	Sequence 28194, A
44	23.2	19.0	734	17	US-10-027-632-28194	Sequence 28194, A
45	23.2	19.0	966	18	US-10-437-963-48653	Sequence 48653, A

ALIGNMENTS

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RESULT 1
US-10-400-053-23
; Sequence 23, Application US/10400053
; Publication No. US20030220286A1
; GENERAL INFORMATION:
; APPLICANT: Adituzzese, Ronald V
; APPLICANT: Mehta, Vidya
; APPLICANT: No. US20030220286A1dctrom, Jeffrey L
; APPLICANT: Fowell, Jason
; APPLICANT: O'Malley, Bert W.
; APPLICANT: Tsai, Sophia
; TITLE OF INVENTION: Improved System for Regulation of Transgene Expression
; FILE REFERENCE: 213-0080US
; CURRENT APPLICATION NUMBER: US/10/400,053
; CURRENT FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: PCT/US01/30305
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/260,781
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/278,281
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,030
; PRIOR FILING DATE: 2000-09-25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 3100
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Complete nucleic acid sequence of pP1666 plasmid.
US-10-400-053-23
Query Match 36.9%, Score 45, DB 17, Length 3100,

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: March 1, 2005, 13:37:48 ; Search time 156.41 Seconds
(without alignments)
1276.296 Million cell updates/sec

Title: US-09-754-014A-13

Perfect score: 122
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Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

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Total number of Hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	25.4	20.8	4602	US-09-149-476-74	Sequence 74, Appl
3	24.6	20.2	2786	US-09-149-476-238	Sequence 238, Appl
4	23.4	19.2	120609	US-09-949-016-13915	Sequence 13915, A
5	23.2	19.0	974	US-09-509-712B-4	Sequence 4, Appl
6	23	18.9	913	US-09-774-528-410	Sequence 410, Appl
7	23	18.9	264665	US-09-949-016-13747	Sequence 13747, A
8	22.8	18.7	1055	US-09-270-767-9711	Sequence 9711, Ap
9	22.8	18.7	1055	US-09-270-767-24993	Sequence 24993, A
10	22.6	18.5	970	US-09-509-712B-122	Sequence 122, Appl
11	22.6	18.5	988	US-09-509-712B-54	Sequence 54, Appl
12	22.4	18.4	4098	US-08-605-106-4	Sequence 4, Appl
13	22.4	18.4	189560	US-09-949-016-17202	Sequence 17202, A
14	22.2	18.2	544	US-09-490-818-2	Sequence 2, Appl
15	22.2	18.2	2860	US-09-543-681A-127	Sequence 127, Appl
16	22.2	18.2	2860	US-09-221-017B-871	Sequence 871, Appl
17	22.2	18.2	22980	US-09-949-016-16145	Sequence 16145, A
18	22.2	18.2	245286	US-09-949-016-15497	Sequence 15497, A
19	22	18.0	601	US-09-949-016-15857	Sequence 15857, A
20	22	18.0	52821	US-09-949-016-146471	Sequence 146471, A
21	22	18.0	52824	US-09-949-016-12116	Sequence 12116, A
22	21.8	17.9	601	US-09-949-016-18015	Sequence 18015, A
23	21.8	17.9	601	US-09-949-016-51591	Sequence 51591, A
24	21.8	17.9	601	US-09-949-016-56814	Sequence 56814, A
25	21.8	17.9	601	US-09-949-016-56815	Sequence 56815, A
26	21.8	17.9	601	US-09-949-016-56816	Sequence 56816, A
27	21.8	17.9	601	US-09-949-016-56817	Sequence 56817, A

28	21.8	17.9	95621	4	US-09-949-016-13237	Sequence 13237, A
29	21.8	17.9	161124	4	US-09-949-016-11760	Sequence 11760, A
30	21.8	17.9	392000	4	US-10-027-983-11	Sequence 11, Appl
31	21.8	17.9	636591	4	US-09-949-016-11808	Sequence 11808, A
32	21.8	17.9	636591	4	US-09-949-016-13388	Sequence 13388, A
33	21.6	17.7	368	4	US-09-513-999C-24491	Sequence 24491, A
34	21.6	17.7	601	4	US-09-949-016-172289	Sequence 172289, A
35	21.6	17.7	79888	4	US-09-949-016-13274	Sequence 13274, A
36	21.6	17.7	79889	4	US-09-949-016-16254	Sequence 16254, A
37	21.6	17.7	106929	4	US-09-949-016-12060	Sequence 12060, A
38	21.6	17.7	106929	4	US-09-949-016-16618	Sequence 16618, A
39	21.6	17.7	155617	4	US-09-949-016-16191	Sequence 16191, A
40	21.6	17.7	254405	4	US-09-949-016-14381	Sequence 14381, A
41	21.4	17.5	601	4	US-09-949-016-179238	Sequence 179238, A
42	21.4	17.5	601	4	US-09-949-016-190619	Sequence 190619, A
43	21.4	17.5	2418	4	US-09-107-532A-2849	Sequence 2849, Ap
44	21.4	17.5	107937	4	US-09-949-016-17192	Sequence 17192, A
45	21.4	17.5	177293	4	US-09-949-016-16513	Sequence 16513, A

ALIGNMENTS

RESULT 1
US-09-012-366-7

; Sequence 7, Application US/09012366
; Patent No. 6034072

; GENERAL INFORMATION:

; APPLICANT: Robert Ralston

; APPLICANT: Susanne Muller

; APPLICANT: Russ Munger

; APPLICANT: William Munger

; APPLICANT: Maria Bruno

; TITLE OF INVENTION: IL-2 GENE EXPRESSION AND

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 MB

; MEDIUM TYPE: storage

; OPERATING SYSTEM: IBM Compatible

; SOFTWARE: FASTSEQ for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/012,366

; FILING DATE: January 23, 1998

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/039,709

; FILING DATE: February 10, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Berkman, Charles S.

; REGISTRATION NUMBER: 38,077

; REFERENCE/DOCKET NUMBER: 230/214

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELETYPE: 67-3510

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-012-366-7

[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 12:40:13 ; Search time 1642.38 Seconds
(without alignments)
1042.930 Million cell updates/sec

Title: US-09-754-014a-10

Perfect score: 45

Sequence: 1 caggttaagtgctctcacta.....tctttctctctcagcag 45

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	25.6	57.8	750	8	BZ061605
6	25.6	57.8	944	9	CL097908
7	25.6	57.8	377	4	BG956291
8	25.6	57.8	608	5	BQ633133
9	25.6	57.8	722	1	AJ813585
10	24.8	55.1	282	2	BB719536
11	24.8	55.1	410	9	CE408506
12	24.8	55.1	417	1	AL653017
13	24.8	55.1	368	1	AV838611
14	24.6	54.7	387	1	AV948860
15	24.6	54.7	544	5	BM174638
16	24.6	54.7	550	5	BM303928
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18	24.6	54.7	603	1	AV858590
19	24.6	54.7	635	8	AZ405316
20	24.6	54.7	678	1	AV843858
21	24.6	54.7	682	5	BM158158
22	24.6	54.7	698	5	BM179050
23	24.6	54.7	698	5	BM269093
24	24.6	54.7	698	5	BM290068

25	24.6	54.7	746	5	BM180524
26	24.6	54.7	748	5	BM424520
27	24.6	54.7	750	5	BM419912
28	24.6	54.7	756	5	BM139250
29	24.6	54.7	761	5	BM085301
30	24.6	54.7	773	5	BM153823
31	24.6	54.7	777	5	BM160591
32	24.6	54.7	779	5	BM498931
33	24.6	54.7	760	8	BZ261009
34	24.6	54.2	777	8	AQ748835
35	24.2	53.8	511	9	CG910690
36	24.2	53.8	603	9	CC695235
37	24.2	53.8	667	9	CB241851
38	24.2	53.8	682	8	AQ855610
39	24.2	53.8	710	5	BU337185
40	24.2	53.8	712	5	CC490080
41	24.2	53.8	890	8	AZ674043
42	24.2	53.8	919	6	CD362421
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ALIGNMENTS

RESULT 1
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DEFINITION XGC-gastrula Xenopus tropicalis cDNA clone Tgaal39m13 5',
AL967706
VERSION AL967706.2 GI:39023831
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 195)
Crotting M.D.R., Ashurst J.L., Taylor R., Zorn A.M. and Rogers J.
Sanger Xenopus tropicalis EST project 2001 (11.2003)
JOURNAL Unpublished (2003)
COMMENT On Nov 27, 2002 this sequence version replaced gi:25791301.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: Tgaal39m13.p1kSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13
gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107, Site 1: EcoRI, Site 2: NotI
Host: Escherichia coli XL1-blue.
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/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="Tgaal39m13"
/dev_stage="gastrula (stages 10-5-12 mixed)"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107, Site 1: EcoRI, Site 2: NotI, cDNA
was oligo dt primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

ORIGIN

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: March 1, 2005, 12:30:33 ; Search time 196.615 Seconds
(without alignments)
1354.870 Million cell updates/sec

Title: US-09-754-014A-10

Perfect score: 45
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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3: geneeqn2000s:*
4: geneeqn2001a:*
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12: geneeqn2004a:*
13: geneeqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	31.4	69.8	160	6	ABQ74561
5	31.4	69.8	160	10	AAZ53803
6	31.4	69.8	5686	2	AAZ40415
7	31.4	69.8	5686	12	ADP77239
8	30	66.7	30	2	AAZ40413
9	30	66.7	30	12	ADP77253
10	30	66.7	3026	10	AAZ53819
11	30	66.7	3100	6	ABN86161
12	30	66.7	3308	12	KD197187
13	30	66.7	3323	12	KD197188
14	30	66.7	3334	12	KD197186
15	30	66.7	3358	2	AAZ40415
16	30	66.7	3358	2	AAZ40418
17	30	66.7	3559	5	AAI10084
18	30	66.7	3559	12	ADP77242
19	30	66.7	3593	5	AAI10085
20	30	66.7	3593	5	AAI10085

21	30	66.7	4276	5	AAI70087
22	30	66.7	4496	5	AAI70086
23	30	66.7	4855	9	AAI60458
24	30	66.7	4855	10	AAZ53818
25	30	66.7	4855	13	ADR23407
26	30	66.7	5195	6	ABQ74554
27	30	66.7	5195	12	ADM94827
28	30	66.7	5566	6	ABN86160
29	30	66.7	5566	2	AAZ40417
30	30	66.7	5966	12	ADP77241
31	28	62.2	86	10	AAZ53801
32	25	55.6	159	12	ADM94833
33	24.6	54.7	1112	12	ADQ08637
34	24.6	54.2	2856	10	ADP47140
35	24	53.3	1234	12	ADL97789
36	23.8	52.9	2283	6	ABQ3434
37	23.6	52.4	110000	2	AAV21209_07
38	23.6	52.4	110000	2	AAV21209_08
39	23.2	51.6	1018	10	ADC86628
40	23.2	51.6	1018	10	ADC86756
41	23	51.1	2356	10	ADP59119
42	23	51.1	125322	13	ABD33622
43	23	51.1	263744	10	ADP08271
44	22.8	50.7	50000	6	AAZ6437
45	22.8	50.7	50000	6	AAZ64400

ALIGNMENTS

RESULT 1	AAV07276	standard; DNA; 45 BP.
ID	AAV07276	
XX	AAV07276	
AC	XX	
XX	XX	
DT	25-SEP-1998	(first entry)
XX	XX	
DE	Plasmid PIN0773 Intron.	
XX	XX	
KM	IL-12 subunit; expression construct; treatment: asthma;	
KW	microbial infection; viral infection; cancer; Human; Interleukin; ss.	
OS	Synthetic.	
XX	XX	
FH	Key	Location/Qualifiers
FT	misc_feature	1..9
FT	misc_feature	/tag= a
FT	misc_feature	/note= "5' splice site"
FT	misc_feature	15..16
FT	misc_feature	/tag= b
FT	misc_feature	/note= "Unspecified sequence of 77 bp not given"
FT	misc_feature	16..22
FT	misc_feature	/tag= c
FT	misc_feature	/note= "Branch point"
FT	misc_feature	25..44
FT	misc_feature	/tag= d
FT	misc_feature	/note= "3' splice site"
PN	MO9817689-42.	
XX	XX	
PD	30-APR-1998.	
XX	XX	
PR	10-OCT-1997;	97NO-US018719.
XX	XX	
PR	18-OCT-1996;	96US-0028616r.
XX	XX	
PR	(GENE-) GENEMEDICINE INC.	
XX	XX	
PR	Notaricum S. Pletmark B.	Designable D.
XX	XX	
DR	WEI, 1998-261A28173.	
XX	XX	

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 13:37:48 ; Search time 57.6923 Seconds
(without alignments)
1276.236 Million cell updates/sec

Title: US-09-754-014a-10

Perfect score: 45
Sequence: 1 caggragagctctctcacta.....tctctctctctcagcag 45

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
4: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
6: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
7: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
8: /cgn2_6/prodata/1/ina/5B_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	66.7	30	US-09-012-366-7	Sequence 7, Appl
2	25.4	56.4	248968	US-09-949-016-12614	Sequence 12614, A
3	25.4	56.4	250958	US-09-949-016-16061	Sequence 16061, A
4	23.8	52.9	601	US-09-949-016-189815	Sequence 189815, A
5	23.8	52.9	601	US-09-949-016-189816	Sequence 189816, A
6	23.6	52.4	1664976	US-09-949-016-17175	Sequence 17175, A
7	23.6	52.4	1664976	US-09-949-016-17175	Sequence 17175, A
8	23.6	52.4	1664976	US-09-949-016-17175	Sequence 17175, A
9	23.6	52.4	1664976	US-09-949-016-17175	Sequence 17175, A
10	22.4	49.8	69062	US-09-949-016-13608	Sequence 13608, A
11	22.4	49.8	69062	US-09-949-016-13608	Sequence 13608, A
12	22.4	49.8	69062	US-09-949-016-13608	Sequence 13608, A
13	22.2	49.3	11325	US-09-436-983-2	Sequence 2, Appl
14	22.2	49.3	11325	US-09-436-983-2	Sequence 2, Appl
15	22.2	49.3	11325	US-09-436-983-2	Sequence 2, Appl
16	22.2	49.3	11325	US-09-436-983-2	Sequence 2, Appl
17	22.2	49.3	11325	US-09-436-983-2	Sequence 2, Appl
18	22.2	49.3	11325	US-09-436-983-2	Sequence 2, Appl
19	22.2	49.3	11325	US-09-436-983-2	Sequence 2, Appl
20	22.2	49.3	11325	US-09-436-983-2	Sequence 2, Appl
21	21.8	48.4	315	US-09-248-796A-12307	Sequence 12307, A
22	21.8	48.4	315	US-09-248-796A-12307	Sequence 12307, A
23	21.8	48.4	315	US-09-248-796A-12307	Sequence 12307, A
24	21.8	48.4	315	US-09-248-796A-12307	Sequence 12307, A
25	21.8	48.4	315	US-09-248-796A-12307	Sequence 12307, A
26	21.8	48.4	315	US-09-248-796A-12307	Sequence 12307, A
27	21.8	48.4	315	US-09-248-796A-12307	Sequence 12307, A

28	21.8	48.4	58829	US-09-949-016-13146	Sequence 13146, A
29	21.8	48.4	87305	US-09-949-016-13430	Sequence 13430, A
30	21.8	48.4	87352	US-09-949-016-12053	Sequence 12053, A
31	21.8	48.4	87352	US-09-949-016-12721	Sequence 12721, A
32	21.8	48.4	87352	US-09-949-016-15693	Sequence 15693, A
33	21.8	48.4	87352	US-09-949-016-15693	Sequence 15693, A
34	21.8	48.4	102520	US-09-949-016-17367	Sequence 17367, A
35	21.8	48.4	102526	US-09-949-016-12448	Sequence 12448, A
36	21.6	48.0	601	US-09-949-016-125939	Sequence 125939, A
37	21.6	48.0	601	US-09-949-016-125940	Sequence 125940, A
38	21.6	48.0	601	US-09-949-016-155936	Sequence 155936, A
39	21.6	48.0	601	US-09-949-016-155937	Sequence 155937, A
40	21.6	48.0	601	US-09-949-016-183364	Sequence 183364, A
41	21.6	48.0	19451	US-09-949-016-13695	Sequence 13695, A
42	21.6	48.0	28494	US-09-949-016-13200	Sequence 13200, A
43	21.6	48.0	47818	US-09-949-016-12324	Sequence 12324, A
44	21.6	48.0	48480	US-09-949-016-15166	Sequence 15166, A
45	21.6	48.0	57638	US-09-949-016-17000	Sequence 17000, A

ALIGNMENTS

RESULT 1
US-09-012-366-7
Sequence 7, Application US/09012366
Patent No. 6034072
GENERAL INFORMATION:
APPLICANT: Robert Ralston
APPLICANT: Susanne Muller
APPLICANT: Russ Mumper
APPLICANT: William Mumper
APPLICANT: Maria Bruno
TITLE OF INVENTION: IL-2 GENE EXPRESSION AND
DELIVERY SYSTEMS AND USES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,366
FILING DATE: January 23, 1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/039,709
FILING DATE: February 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Berkman, Charles S.
REGISTRATION NUMBER: 38,077
REFERENCE/DOCKET NUMBER: 230/214
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO.: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-012-366-7